

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS

- sub b) 1 A method for detecting methylated nucleic acids comprising the steps of:
- 5 (i) contacting a nucleic acid sample suspected of containing methylated nucleotides with an oligonucleotide sequence under suitable conditions for nucleic acid hybridization, said oligonucleotide sequence characterised in that,
- 10 (a) it comprises a first stem labeled with a fluorophore moiety, a loop sequence having a region of nucleotides complementary to at least a region of the nucleic acid sample, which region is susceptible to methylation, and a second stem labeled with a quencher moiety that is capable of quenching the fluorophore moiety when in spatial proximity to the fluorophore moiety; and
- 15 (b) the nucleotides forming the first stem are capable of moving into spatial proximity with the nucleotides forming the second stem when the probe is dissociated from the nucleic acid sample;
- (ii) altering the hybridization conditions such that the oligonucleotide probe dissociates from unmethylated DNA but remains hybridized to methylated DNA; and
- (iii) measuring the change in fluorescence
- 20 2 A method according to claim 1 wherein when the labeled oligonucleotide sequences dissociate from the target nucleic acid sample according to step (ii) the first and second stem hybridise together causing quenching of the fluorophore moiety.
- 3 A method according to claim 1 wherein the loop sequence contains at least
- 25 about 10 nucleotides.
- 4 A method according to claim 1 wherein the loop sequence contains at least about up to 35 nucleotides.
- 5 A method according to claim 1 wherein the loop sequence contains at least about 25 nucleotides.

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A method according to claim 1 wherein the loop sequence contains at least about from 15-20 nucleotides.

7 A method according to claim 1 wherein when the loop sequence is complementary to a portion of a nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

8 A method according to claim 1 wherein when the loop sequence is complementary to a portion of a Myf-3 nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

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A method according to claim 8 wherein the labelled oligonucleotide sequence is complementary to at least one of the sequences selected from the group consisting of:

- group consisting of:
- (i) 5' GCG GCG ACT CCG ACG CGT CCA GCC CGC GCT CC 3'
 - (ii) 5' TTA TAC CGC AGG CGG GCG AGC CGC GGG CGC TCG CT 3'
 - (iii) 5' CCG AGA GCC CTG CGG GGC CCG CCC TCC TGC TGG CG 3'

15 10 A method according to claim 1 wherein when the loop sequence is complementary to a portion of a glutathione-S-transferase- Π (pi) nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

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11 A method according to claim 10 wherein the labelled oligonucleotide sequence is complementary to at least one of the sequences selected from the group consisting of:

- the group consisting of:
- i) 5' CTC CAG CGA AGG CCT CGC GGC CTC CGA GGC TTA TAA G 3'
 - ii) 5' GGG GAC GCG GGC CGC GCG TAC TCA CTG GTG GCG A 3'

12 A method according to claim 1 wherein when the loop sequence is
25 complementary to a portion of a calcitonin nucleic acid sequence that
undergoes methylation when a cell transforms from a normal state to a
cancerous state.

13 A method according to claim 1 wherein the method is used to detect abnormally methylated gene sequences in prostate cancer tissues.

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